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ARTICLE

NMR assignments of the WBSCR27 protein related to Williams-Beuren syndrome

Sofia S. Mariasina[1,2] · Olga A. Petrova[3] · Ilya A. Osterman[2,3,4] · Olga V. Sergeeva[4] · Sergey V. Efimov[5] · Vladimir V. Klochkov[5] · Petr V. Sergiev[2,3,4] · Olga A. Dontsova[2,3,4] · Tai-huang Huang[6] · Chi-Fon Chang[7] · Vladimir I. Polshakov[1]

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Abstract

Williams-Beuren syndrome is a genetic disorder characterized by physiological and mental abnormalities, and is caused by hemizygous deletion of several genes in chromosome 7. One of the removed genes encodes the WBSCR27 protein. Bioinformatic analysis of the sequence of WBSCR27 indicates that it belongs to the family of SAM-dependent methyltransferases. However, exact cellular functions of this protein or phenotypic consequences of its deficiency are still unknown. Here we report nearly complete ^{1}H, ^{15}N, and ^{13}C chemical shifts assignments of the 26 kDa WBSCR27 protein from *Mus musculus* in complex with the cofactor *S*-adenosyl-L-methionine (SAM). Analysis of the assigned chemical shifts allowed us to characterize the protein's secondary structure and backbone dynamics. The topology of the protein's fold confirms the assumption that the WBSCR27 protein belongs to the family of class I methyltransferases.

Keywords SAM-dependent methyltransferases · Williams-Beuren syndrome · Protein NMR · Resonance assignment · Secondary structure

✉ Chi-Fon Chang
chifon@gate.sinica.edu.tw

✉ Vladimir I. Polshakov
vpolsha@mail.ru

1 Faculty of Fundamental Medicine, Center for Magnetic Tomography and Spectroscopy, M.V. Lomonosov Moscow State University, Moscow, Russia 119991

2 Department of Chemistry, M.V. Lomonosov Moscow State University, Moscow, Russia 119991

3 A.N. Belozersky Institute of Physico-Chemical Biology, M.V. Lomonosov Moscow State University, Moscow, Russia 119991

4 Skolkovo Institute of Science and Technology, Moscow, Russia

5 NMR Laboratory, Institute of Physics, Kazan Federal University, 18 Kremlevskaya, Kazan, Russia 420008

6 Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan, Republic of China

7 Genomics Research Center, Academia Sinica, Taipei, Taiwan, Republic of China

Abbreviations

SAM	*S*-Adenosyl-L-methionine
TEV	Tobacco Etch Virus nuclear-inclusion-a endopeptidase
WBS	Williams-Beuren syndrome
WBSCR	Williams-Beuren syndrome chromosome region
WBSCR27	Williams-Beuren Syndrome Chromosome Region 27 protein

Biological context

Protein WBSCR27 is encoded in the chromosome 7q11.23 region that is associated with Williams-Beuren Syndrome (WBS) (Strømme et al. 2002)—a rare genetic disorder (~ 1 in 7500 live births) characterized by physiological and mental problems. WBS patients suffer from cardiovascular abnormalities—stenosis of medium and large arteries, dysfunctions of the endocrine system—mostly calcium abnormalities (hypercalcemia) and thyroid abnormalities (hypothyroidism). WBS also causes a set of neurodevelopmental disturbances causing developmental and cognitional delays, and characteristic social behavior manifested